

Online Bioinformatics Training Workshop Schedule and Assignments December 7 – 17, 2020, 11:00AM – 1:00PM

Note: Some of the reading assignments refer to a section in the guide with multiple pages. Participants should read all of the pages in the assigned section.

*Annotation Outline is an outline of much of the rest of the guide and is intended to be a quick reference. You are not responsible for reading all of the linked pages in this section; merely note the organization.

Week 1

Day	Live Sessions	Pre-live Session Readings	Short Videos	Tasks
1	<ul style="list-style-type: none"> Welcome and Overview 	<ul style="list-style-type: none"> Introduction Annotation Outline Genome annotation Overview Decision Trees Mechanics: Part 1(through "Generating a rough draft...) 	<ul style="list-style-type: none"> Setting DNA Master Preferences Autoannotation BLASTing your genome in DNA Master Saving your DNA Master file 	<ul style="list-style-type: none"> Auto-annotate and then BLAST Gandalf20 in DNA Master Save File
2	<ul style="list-style-type: none"> Genome Overview Compare genomes using Phamerator Compare using BLASTN on phagesdb.org 	<ul style="list-style-type: none"> Guiding principles Mechanics: Phamerator Mechanics: Other 	<ul style="list-style-type: none"> Phagesdb tour Phamerator overview GeneMark output Aragorn output tRNAscanSE output 	<ul style="list-style-type: none"> Generate GeneMark S and GeneMark host files Generate Aragorn and tRNAscanSE outputs. Phamerator map of Gandalf20 and others
3	<ul style="list-style-type: none"> Call genes 6-12 Choosing starts 	<ul style="list-style-type: none"> Evaluating gene predictions Evaluating gene starts Mechanics: DNA Master 	<ul style="list-style-type: none"> Using Starterator GeneMark output overview Other how-to DNA Master videos 	<ul style="list-style-type: none"> Call genes 13-30 in DNA Master.
4	<ul style="list-style-type: none"> Functions Review first 30 genes (participant's choice) Call some reverse genes 	<ul style="list-style-type: none"> Bacteriophage Biology Predicting Phage Gene Functions Cluster specific forums Official Function List Databases 	<ul style="list-style-type: none"> Using HHPred SEA-PHAGES Forums tour 	<ul style="list-style-type: none"> As many as you can call

5	<ul style="list-style-type: none"> Office hours 	<ul style="list-style-type: none"> Predicting tRNAs Documenting your annotation Case Studies 	<ul style="list-style-type: none"> Frameshift tRNAs 	<ul style="list-style-type: none"> As many genes as you can call
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Week 2

6	<ul style="list-style-type: none"> Sequencing Black Box/What's in a name? Review of genes (participant choice) tRNAs Frameshifts 	<ul style="list-style-type: none"> Reviewing Gaps Quality control Bioinformatics Basics Programs 	<ul style="list-style-type: none"> Checking the gaps Make genome profile 	<ul style="list-style-type: none"> Finish genome Make genome profile
7	<ul style="list-style-type: none"> Difficult genes/features (PC) Revisit notes 	<ul style="list-style-type: none"> Last Call Submitting your files to phagesdb How to pass preliminary QC 		<ul style="list-style-type: none"> Finish genome
8	<ul style="list-style-type: none"> Graham File submissions Investigating clusters PECAAN 	<ul style="list-style-type: none"> PECAAN 	<ul style="list-style-type: none"> Making your submission files Submitting your annotation 	<ul style="list-style-type: none"> Generate the files for file submission
9	<ul style="list-style-type: none"> Annotation QC— behind the scenes Review to Improve Where and when to ask questions Pedagogy 	<ul style="list-style-type: none"> SEA-PHAGES forums Review to Improve 	<ul style="list-style-type: none"> Review to Improve 	<ul style="list-style-type: none"> Review to improve Classroom Implementation